

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/819,669DDATE: 10/08/1999
TIME: 13:48:03

INPUT SET: S33581.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

- (i) APPLICANTS: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
- (ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
Rejection Antigens and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Fulbright & Jaworski LLP
(B) STREET: 666 Fifth Avenue
(C) CITY: New York City
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10103
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
(B) COMPUTER: IBM
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/819,669
(B) FILING DATE: 17-March-1997
(C) CLASSIFICATION: 435
- (vii) PRIOR APPLIATION DATA:
(A) APPLICATION NUMBER: 08/142,368
(B) FILING DATE: 02-MAY-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US92/04354
(B) FILING DATE: 22-MAY-1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/807,043
(B) FILING DATE: 12-DECEMBER-1991
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/764,364

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47 (B) FILING DATE: 23-SEPTEMBER-1991
48
49 (vii) PRIOR APPLICATION DATA:
50 (A) APPLICATION NUMBER: 07/728,838
51 (b) FILING DATE: 9-JULY-1991
52
53 (vii) PRIOR APPLICATION DATA:
54 (A) APPLICATION NUMBER: 07/705,702
55 (B) FILING DATE: 23-May-1991
56
57 (viii) ATTORNEY/AGENT INFORMATION:
58 (A) NAME: Hanson, Norman D.
59 (B) REGISTRATION NUMBER: 30,946
60 (C) REFERENCE/DOCKET NUMBER: LUD 5253.5-US
61
62 (ix) TELECOMMUNICATION INFORMATION:
63 (A) TELEPHONE: (212)318-3168
64 (B) TELEFAX: (212)752-5958
65
66
67

68 (2) INFORMATION FOR SEQ ID NO: 1:
69 (i) SEQUENCE CHARACTERISTICS:
70 (A) LENGTH: 462 base pairs
71 (B) TYPE: nucleic acid
72 (C) STRANDEDNESS: single
73 (D) TOPOLOGY: linear
74 (ii) MOLECULE TYPE: genomic DNA
75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
76
77
78
79

80	ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG	60
81	ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT	120
82	CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG	180
83	CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC	240
84	CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT	300
85	AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG CATGCATTGT	360
86	GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT	420
87	TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC	462

88
89
90
91

92 (2) INFORMATION FOR SEQ ID NO: 2:
93 (i) SEQUENCE CHARACTERISTICS:
94 (A) LENGTH: 675 base pairs
95 (B) TYPE: nucleic acid
96 (C) STRANDEDNESS: single
97 (D) TOPOLOGY: linear
98 (ii) MOLECULE TYPE: genomic DNA
99 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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102 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT      48
103 Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
104                               5                               10                               15
105 GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA      96
106 Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
107                               20                               25                               30
108 GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA      144
109 Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
110                               35                               40                               45
111 AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG      192
112 Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
113                               50                               55                               60
114 TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC      240
115 Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
116                               65                               70                               75                               80
117 TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC      288
118 Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
119                               85                               90                               95
120 GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT      336
121 Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
122                               100                              105                              110
123 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG      384
124 Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
125                               115                              120                              125
126 GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG      432
127 Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
128                               130                              135                              140
129 GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG      480
130 Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
131                               145                              150                              155                              160
132 AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC CAC GAC CCT AAT TTC      528
133 Asn Glu Val Lys Cys Arg Met Ile Tyr Phe His Asp Pro Asn Phe
134                               165                              170                              175
135 CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT      576
136 Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
137                               180                              185                              190
138 GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG      624
139 Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu
140                               195                              200                              210
141 GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT      672
142 Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
143                               220                              225                              230                              235
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145 TAG      675
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148
149 (2) INFORMATION FOR SEQ ID NO: 3:
150     (i) SEQUENCE CHARACTERISTICS:
151         (A) LENGTH: 228 base pairs
152         (B) TYPE: nucleic acid

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153 (C) STRANDEDNESS: single
154 (D) TOPOLOGY: linear
155 (ii) MOLECULE TYPE: genomic DNA
156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
157
158
159
160 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT 60
161 TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT 120
162 TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACCTT CATATGATAC 180
163 ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC 228
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165
166 (2) INFORMATION FOR SEQ ID NO: 4:
167 (i) SEQUENCE CHARACTERISTICS:
168 (A) LENGTH: 1365 base pairs
169 (B) TYPE: nucleic acid
170 (C) STRANDEDNESS: single
171 (D) TOPOLOGY: linear
172 (ii) MOLECULE TYPE: genomic DNA
173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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175
176 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT 50
177 GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT 100
178 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG 150
179 AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT 200
180 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250
181 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
182 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG 350
183 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG 400
184 CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT 450
185 ACCCTTTGTG CC 462
186 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
187 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
188 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588
189 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
190 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
191 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
192 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC 756
193 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798
194 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840
195 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
196 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT 924
197 GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT 966
198 TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG 1008
199 AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT 1050
200 GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG 1092
201 GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 1134
202 TAG 1137
203 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG 1187
204 TTGTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA 1237
205 ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT 1287

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206	CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT	1337
207	GTTAAAAATA AAAGTTTGAC TTGCATAC	1365
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211	(2) INFORMATION FOR SEQ ID NO: 5:	
212	(i) SEQUENCE CHARACTERISTICS:	
213	(A) LENGTH: 4698 base pairs	
214	(B) TYPE: nucleic acid	
215	(C) STRANDEDNESS: single	
216	(D) TOPOLOGY: linear	
217	(ii) MOLECULE TYPE: genomic DNA	
218	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
219		
220	ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT	50
221	GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT	100
222	CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG	150
223	AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT	200
224	CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCA	250
225	CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT	300
226	AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG	350
227	CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG	400
228	CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT	450
229	ACCCCTTGTG CC	462
230	ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA	504
231	GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG	546
232	TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	588
233	TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	630
234	ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
235	TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
236	GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC	756
237	GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	798
238	GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA	840
239	GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
240	GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T	916
241	GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA	966
242	CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC	1016
243	TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC	1066
244	CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG CCTCTGGAGC	1116
245	TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC	1166
246	TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCTC	1216
247	TTCAGGCTTC CCCATTGTCT CCTCTCCCGA AACCCCTCCCC TTCCTGTTCC	1266
248	CCTTTTCGCG CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT	1316
249	TCACCAGCTT TGCTCTCCCT GCTCCCCCTC CCCTTTTGCA CCTTTTCTTT	1366
250	TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT	1416
251	CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCGGG	1466
252	TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT	1516
253	CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT	1566
254	TTGGTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTGGCT GTCCTGGCAC	1616
255	TCACTCTGTA GACCAGGCTG GCCTCAAAC CAGAAATCTG CCTGCCTCTG	1666
256	CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCAGTGCAG	1716
257	GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT TCTGCATGTT	1766
258	AACTCCCTTT TTGGCACCTT TCCTTTACAG GACCCCTCC CCCTCCCTGT	1816

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***** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

398 (2) INFORMATION FOR SEQ ID NO: 8:
399 (i) SEQUENCE CHARACTERISTICS:
400 (A) LENGTH: 5674 base pairs
401 (B) TYPE: nucleic acid
402 (C) STRANDEDNESS: single
403 (D) TOPOLOGY: linear
404 (ii) MOLECULE TYPE: genomic DNA
405 (ix) FEATURE:
406 (A) NAME/KEY: MAGE-1 gene
407 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
408
409
410 CCCGGGGCAC CACTGGCATC CCTCCCCCTA CCACCCCCAA TCCCTCCCTT 50
411 TACGCCACCC ATCCAAACAT CTTCACGCTC ACCCCCAGCC CAAGCCAGGC 100
412 AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAGCCC AGGTGCCCAG 150
413 ATGTGACGCC ACTGACTTGA GCATTAGTGG TTAGAGAGAA GCGAGGTTTT 200
414 CGGTCTGAGG GCGCGCTTGA GATCGGTGGA GGGGAAGCGGG CCCAGCTCTG 250
415 TAAGGAGGCA AGGTGACATG CTGAGGGAGG ACTGAGGACC CACTTACCCC 300
416 AGATAGAGGA CCCCAAATA TCCCTTCATG CCAGTCTTGG ACCATCTGGT 350
417 GGTGGACTTC TCAGGCTGGG CCACCCCCAG CCCCCTTGCT GCTTAAACCA 400
418 CTGGGGACTC GAAGTCAGAG CTCCGTGTGA TCAGGGAAGG GCTGCTTAGG 450
419 AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAGG 500
420 AGGGCTGAGG GTCCCTAAGA CCCCCTCCC GTGACCCAAC CCCCCTCCA 550
421 ATGCTCACTC CCGTGACCCA ACCCCCTCTT CATTGTCTATT CCAACCCCCA 600
422 CCCCACATCC CCCACCCCAT CCCTCAACCC TGATGCCCAT CCGCCCAGCC 650
423 ATTCCACCCT CACCCCCACC CCCACCCCCA CGCCCCTCC CACCCCCACC 700
424 CAGGCAGGAT CCGGTTCCCG CCAGGAAACA TCCGGGTGCC CGGATGTGAC 750
425 GCCACTGACT TGCGCATTGT GGGGCAGAGA GAAGCAGGT TTCCATTCTG 800
426 AGGGACGGCG TAGAGTTCGG CCGAAGGAAC CTGACCCAGG CTCTGTGAGG 850
427 AGGCAAGGTG AGAGGCTGAG GGAGGACTGA GGACCCCGCC ACTCCAAATA 900
428 GAGAGCCCCA AATATTCCAG CCCCGCCCTT GCTGCCAGCC CTGGCCCACC 950
429 CGCGGGAAGA CGTCTCAGCC TGGGCTGCCC CCAGACCCCT GCTCCAAAAG 1000
430 CCTTGAGAGA CACCAGGTTT TTCTCCCCAA GCTCTGGAAT CAGAGGTTGC 1050
431 TGTGACCAGG GCAGGACTGG TTAGGAGAGG GCAGGGCACA GGCTCTGCCA 1100
432 GGCATCAAGA TCAGCACCCA AGAGGGAGGG CTGTGGGCCC CCAAGACTGC 1150
433 ACTCCAATCC CCACTCCCAC CCCATTGCA TTCCATTCC CCACCCAACC 1200
434 CCCATCTCCT CAGCTACACC TCCACCCCCA TCCCTACTCC TACTCCGTCA 1250
435 CCTGACCACC ACCCTCCAGC CCCAGCACA GCCCAACCC TTCTGCCACC 1300
436 TCACCTCAC TGCCCCCAAC CCCACCCTCA TCTCTCTCAT GTGCCCCACT 1350
437 CCCATCGCCT CCCCCATTCT GGCAGAATCC GGTTTGCCCC TGCTCTCAAC 1400
438 CCAGGGAAGC CCTGGTAGGC CCGATGTGAA ACCACTGACT TGAACCTCAC 1450
439 AGATCTGAGA GAAGCCAGGT TCATTTAATG GTTCTGAGGG GCGGCTTGAG 1500
440 ATCCACTGAG GGGAGTGGTT TTAGGCTCTG TGAGGAGGCA AGGTGAGATG 1550
441 CTGAGGGAGG ACTGAGGAGG CACACACCCC AGGTAGATGG CCCCAAAATG 1600
442 ATCCAGTACC ACCCTGCTG CCAGCCCTGG ACCACCCGGC CAGGACAGAT 1650
443 GTCTCAGCTG GACCACCCCC CGTCCCGTCC CACTGCCACT TAACCCACAG 1700
444 GGCAATCTGT AGTCATAGCT TATGTGACCG GGGCAGGGTT GGTGAGGAGA 1750

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446	ACCCTGGGAG	GGAAGTGAAG	GTTCCCCACC	CACACCTGTC	TCCTCATCTC	1850
447	CACCGCCACC	CCACTCACAT	TCCCATACCT	ACCCCTTACC	CCCAACCTCA	1900
448	TCTTGTCAGA	ATCCCTGCTG	TCAACCCACG	GAAGCCACGG	GAATGGCGGC	1950
449	CAGGCACTCG	GATCTTGACG	TCCCCATCCA	GGTCTGATG	GAGGGAAGGG	2000
450	GCTTGAACAG	GGCCTCAGGG	GAGCAGAGGG	AGGGCCCTAC	TGCGAGATGA	2050
451	GGGAGGCCTC	AGAGGACCCA	GCACCCTAGG	ACACCGCACC	CCTGTCTGAG	2100
452	ACTGAGGCTG	CCACTTCTGG	CCTCAAGAAT	CAGAACGATG	GGGACTCAGA	2150
453	TTGCATGGGG	GTGGGACCCA	GGCCTGCAAG	GCTTACGCGG	AGGAAGAGGA	2200
454	GGGAGGACTC	AGGGGACCTT	GGAATCCAGA	TCAGTGTGGA	CCTCGGCCCT	2250
455	GAGAGGTCCA	GGGCACGGTG	GCCACATATG	GCCCATATTT	CCTGCATCTT	2300
456	TGAGGTGACA	GGACAGAGCT	GTGGTCTGAG	AAGTGGGGCC	TCAGGTCAAC	2350
457	AGAGGGAGGA	GTTCCAGGAT	CCATATGGCC	CAAGATGTGC	CCCCTTCATG	2400
458	AGGACTGGGG	ATATCCCCGG	CTCAGAAAGA	AGGGACTCCA	CACAGTCTGG	2450
459	CTGTCCCTTC	TTAGTAGCTC	TAGGGGGACC	AGATCAGGGA	TGGCGGTATG	2500
460	TTCCATTCTC	ACTTGTACCA	CAGGCAGGAA	GTTGGGGGGC	CCTCAGGGAG	2550
461	ATGGGGTCTT	GGGGTAAAGG	GGGGATGTCT	ACTCATGTCA	GGGAATTGGG	2600
462	GGTTGAGGAA	GCACAGGCGC	TGGCAGGAAT	AAAGATGAGT	GAGACAGACA	2650
463	AGGCTATTGG	AATCCACACC	CCAGAACCAA	AGGGGTGAGC	CCTGGACACC	2700
464	TCACCCAGGA	TGTGGCTTCT	TTTTCACTCC	TGTTTTCCAGA	TCTGGGGCAG	2750
465	GTGAGGACCT	CATTCTCAGA	GGGTGACTCA	GGTCAACGTA	GGGACCCCCA	2800
466	TCTGGTCTAA	AGACAGAGCG	GTCCCAGGAT	CTGCCATGCG	TTCGGGTGAG	2850
467	GAACATGAGG	GAGGACTGAG	GGTACCCCCAG	GACCAGAACA	CTGAGGGAGA	2900
468	CTGCACAGAA	ATCAGCCCTG	CCCCTGCTGT	CACCCAGAG	AGCATGGGCT	2950
469	GGGCCGTCTG	CCGAGGTCCCT	TCCGTTATCC	TGGGATCATT	GATGTCAGGG	3000
470	ACGGGGAGGC	CTTGGTCTGA	GAAGGCTGCG	CTCAGGTCAG	TAGAGGGAGC	3050
471	GTCCAGGCC	CTGCCAGGAG	TCAAGGTGAG	GACCAAGCGG	GCACCTCACC	3100
472	CAGGACACAT	TAATTCCAAT	GAATTTTGAT	ATCTCTTGCT	GCCCTTCCCC	3150
473	AAGGACCTAG	GCACGTGTGG	CCAGATGTTT	GTCCCCTCCT	GTCCTTCCAT	3200
474	TCCTTATCAT	GGATGTGAAC	TCTTGATTGG	GATTTCTCAG	ACCAGCAAAA	3250
475	GGGCAGGATC	CAGGCCCTGC	CAGGAAAAAT	ATAAGGGCCC	TGCGTGAGAA	3300
476	CAGAGGGGGT	CATCCACTGC	ATGAGAGTGG	GGATGTCACA	GAGTCCAGCC	3350
477	CACCTCCTTG	GTAGCACTGA	GAAGCCAGGG	CTGTGCTTGC	GGTCTGCACC	3400
478	CTGAGGGCCC	GTGGATTCCCT	CTTCCTGGAG	CTCCAGGAAC	CAGGCAGTGA	3450
479	GGCCTTGGTG	TGAGACAGTA	TCCTCAGGTC	TGACAGCAGA	GGATGCACAG	3500
480	GGTGTGCCAG	CAGTGAATGT	TTGCCCTGAA	ATCAGACCAA	GGGCCCCACC	3550
481	TGCCACAGGA	CACATAGGAC	TCCACAGAGT	CTGGCCTCAC	CTCCCTACTG	3600
482	TCAGTCCTGT	AGAATCGACC	TCTGCTGGCC	GGCTGTACCC	TGAGTACCCT	3650
483	CTCACTTCCT	CCTTCAGGTT	TTCAGGGGAC	AGGCCAACCC	AGAGGACAGG	3700
484	ATTCCCTGGA	GGCCACAGAG	GAGCACCAG	GAGAAGATCT	GTAAGTAGGC	3750
485	CTTTGTAGTA	GTCTCCAAGG	TTCAGTTCTC	AGCTGAGGCC	TCTCACACAC	3800
486	TCCCTCTCTC	CCCAGGCCTG	TGGGTCTTCA	TTGCCCAGCT	CCTGCCCACA	3850
487	CTCCTGCCTG	CTGCCCTGAC	GAGAGTCATC			3880
488	ATG TCT CTT	GAG CAG AGG	AGT CTG CAC	TGC AAG	CCT GAG GAA	3922
489	GCC CTT GAG	GCC CAA CAA	GAG GCC CTG	GGC CTG	GTG TGT GTG	3964
490	CAG GCT GCC	ACC TCC TCC	TCT CTT	CTG GTC	CTG GGC ACC	4006
491	CTG GAG GAG	GTG CCC ACT	GCT GGG TCA	ACA GAT	CCT CCC CAG	4048
492	AGT CCT CAG	GGA GCC TCC	GCC TTT CCC	ACT ACC	ATC AAC TTC	4090
493	ACT CGA CAG	AGG CAA CCC	AGT GAG GGT	TCC AGC	AGC CGT GAA	4132
494	GAG GAG GGG	CCA AGC ACC	TCT TGT ATC	CTG GAG	TCC TTG TTC	4174
495	CGA GCA GTA	ATC ACT AAG	AAG GTG GCT	GAT TTG	GTT GGT TTT	4216
496	CTG CTC CTC	AAA TAT CGA	GCC AGG GAG	CCA GTC	ACA AAG GCA	4258
497	GAA ATG CTG	GAG AGT GTC	ATC AAA AAT	TAC AAG	CAC TGT TTT	4300

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498	CCT GAG ATC TTC GGC AAA GCC TCT GAG TCC TTG CAG CTG GTC	4342
499	TTT GGC ATT GAC GTG AAG GAA GCA GAC CCC ACC GGC CAC TCC	4384
500	TAT GTC CTT GTC ACC TGC CTA GGT CTC TCC TAT GAT GGC CTG	4426
501	CTG GGT GAT AAT CAG ATC ATG CCC AAG ACA GGC TTC CTG ATA	4468
502	ATT GTC CTG GTC ATG ATT GCA ATG GAG GGC GGC CAT GCT CCT	4510
503	GAG GAG GAA ATC TGG GAG GAG CTG AGT GTG ATG GAG GTG TAT	4552
504	GAT GGG AGG GAG CAC AGT GCC TAT GGG GAG CCC AGG AAG CTG	4594
505	CTC ACC CAA GAT TTG GTG CAG GAA AAG TAC CTG GAG TAC GGC	4636
506	AGG TGC CGG ACA GTG ATC CCG CAC GCT ATG AGT TCC TGT GGG	4678
507	GTC CAA GGG CCC TCG CTG AAA CCA GCT ATG TGA	4711
508	AAGTCCTTGA GTATGTGATC AAGGTCAGTG CAAGAGTTC	4750
509	GCTTTTCTT CCCATCCCTG CGTGAAGCAG CTTTGAGAGA GGAGGAAGAG	4800
510	GGAGTCTGAG CATGAGTTGC AGCCAAGGCC AGTGGGAGGG GGACTGGGCC	4850
511	AGTGCACCTT CCAGGGCCGC GTCCAGCAGC TTCCCCTGCC TCGTGTGACA	4900
512	TGAGGCCCAT TCTTCACTCT GAAGAGAGCG GTCAGTGTTT TCAGTAGTAG	4950
513	GTTTCTGTTC TATTGGGTGA CTTGGAGATT TATCTTTGTT CTCTTTTGGA	5000
514	ATTGTTCAAA TGTTTTTTTT TAAGGGATGG TTGAATGAAC TTCAGCATCC	5050
515	AAGTTTATGA ATGACAGCAG TCACACAGTT CTGTGTATAT AGTTTAAGGG	5100
516	TAAGAGTCTT GTGTTTTATT CAGATTGGGA AATCCATTCT ATTTTGTGAA	5150
517	TTGGGATAAT AACAGCAGTG GAATAAGTAC TTAGAAATGT GAAAAATGAG	5200
518	CAGTAAATA GATGAGATAA AGAACTAAAG AAATTAAGAG ATAGTCAATT	5250
519	CTTGCCCTTAT ACCTCAGTCT ATTCTGTAAA ATTTTAAAG ATATATGCAT	5300
520	ACCTGGATTT CTTGGCTTC TTTGAGAATG TAAGAGAAAT TAAATCTGAA	5350
521	TAAAGAATTC TTCCTGTTCA CTGGCTCTTT TCTTCTCCAT GCACTGAGCA	5400
522	TCTGCTTTT GGAAGGCCCT GGGTTAGTAG TGGAGATGCT AAGGTAAGCC	5450
523	AGACTCATAG CCACCCATAG GGTCTAGAG TCTAGGAGCT GCAGTCACGT	5500
524	AATCGAGGTG GCAAGATGTC CTCTAAAGAT GTAGGGAAAA GTGAGAGAGG	5550
525	GGTGAGGGTG TGGGGCTCCG GGTGAGAGTG GTGGAGTGTC AATGCCCTGA	5600
526	GCTGGGGCAT TTTGGGCTTT GGGAAACTGC AGTTCCTTCT GGGGGAGCTG	5650
527	ATTGTAATGA TCTTGGGTGG ATCC	5674
528		
529		
530		

1003 (2) INFORMATION FOR SEQ ID NO: 17:
1004 (i) SEQUENCE CHARACTERISTICS:
1005 (A) LENGTH: 2305 base pairs
1006 (B) TYPE: nucleic acid
1007 (C) STRANDEDNESS: single
1008 (D) TOPOLOGY: linear
1009 (ii) MOLECULE TYPE: genomic DNA
1010 (ix) FEATURE:
1011 (A) NAME/KEY: MAGE-51 gene
1012 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

1013		
1014		
1015		
1016	GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG	50
1017	GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC	100
1018	TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG	150
1019	GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT	200
1020	TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC	250
1021	TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC	300

RAW SEQUENCE LISTING
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1024	CTCACTTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG	450
1025	GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG	500
1026	ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTTCAGT TTTTAGCTGA	550
1027	GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC	600
1028	AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC	644
1029	ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA	686
1030	GGC CTT GAC ACC CAA GAA GAG CCC TGG GCC TGG TGG GTG TGC	728
1031	AGG CTG CCA CTA CTG AGG AGC AGG AGG CTG TGT CCT CCT CCT	770
1032	CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG	812
1033	GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA	854
1034	TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA	896
1035	AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC	938
1036	CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG	980
1037	TGG CTG ACT TGA	992
1038	TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCCGGT CACAAAGGCA	1042
1039	GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT	1092
1040	CTTCGGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA	1142
1041	AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA	1192
1042	CTCCTATGAT GGCCTGGTGG TTTAATCAGA TCATGCCCAA GACGGGCCTC	1242
1043	CTGATAATCG TCTTGGGCAT GATTGCAATG GAGGGCAAAT GCGTCCCTGA	1292
1044	GCACAAAATC TGGGAGGAGC TGGGTGTGAT GAAGGTGTAT GTTGGGAGGG	1342
1045	AGCAGAGTGT CTGTGGGGAG CCCAGGAAGC TGCTCACCCA AGATTTGGTG	1392
1046	CAGGAAAATC ACCTGGAGTA CCGCAGGTGC CCAGCAGTGA TCCCATATGC	1442
1047	TATGAGTTAC TGTGGGGTCC AAGGGCACTC GCTGCTTGAA AGTACTGGAG	1492
1048	CACGTGGTCA GGGTCAATGC AAGAGTTCTC ATTTCTTACC CATCCCTGCA	1542
1049	TGAAGCAGCT TTGAGAGAGG AGGAAGAGGG AGTCTGAGCA TGAGCTGCAG	1592
1050	CCAGGGCCAC TGCGAGGGGG GCTGGGCCAG TGCACCTTCC AGGGCTCCGT	1642
1051	CCAGTAGTTT CCCCTGCCTT AATGTGACAT GAGGCCCAT TTTCTCTCTT	1692
1052	TGAAGAGAGC AGTCAACATT CTTAGTAGTG GGTTTCTGTT CTATTGGATG	1742
1053	ACTTTGAGAT TTGTCTTTGT TTCCTTTTGG AATTGTTCAA ATGTTCTTTT	1792
1054	TAATGGGTGG TTGAATGAAC TTCAGCATTC AAATTTATGA ATGACAGTAG	1842
1055	TCACACATAG TGCTGTTTAT ATAGTTTAGG AGTAAGAGTC TTGTTTTTTA	1892
1056	TTCAGATTGG GAAATCCATT CCATTTTGTG AATTGGGACA TAGTTACAGC	1942
1057	AGTGGAATAA GTATTCATTT AGAAATGTGA ATGAGCAGTA AACTGATGA	1992
1058	GATAAAGAAA TTAAAAGATA TTTAATTCTT GCCTTATACT CAGTCTATTC	2042
1059	GGTAAAATTT TTTTTTAAAA ATGTGCATAC CTGGATTTCC TTGGCTTCTT	2092
1060	TGAGAATGTA AGACAAATTA AATCTGAATA AATCATTTCT CCTGTTCACT	2142
1061	GGCTCATTTA TTCTCTATGC ACTGAGCATT TGCTCTGTGG AAGGCCCTGG	2192
1062	GTTAATAGTG GAGATGCTAA GGTAAGCCAG ACTCACCCCT ACCCACAGGG	2242
1063	TAGTAAAGTC TAGGAGCAGC AGTCATATAA TTAAGGTGGA GAGATGCCCT	2292
1064	CTAAGATGTA GAG	2305
1065		
1066		
1067		
1068		

1328 (2) INFORMATION FOR SEQ ID NO: 24:
1329 (i) SEQUENCE CHARACTERISTICS:
1330 (A) LENGTH: 2150 base pairs
1331 (B) TYPE: nucleic acid
1332 (C) STRANDEDNESS: single

RAW SEQUENCE LISTING PATENT APPLICATION US/08/819,669D

DATE: 10/08/1999
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1333         (D) TOPOLOGY: linear
1334         (ii) MOLECULE TYPE: genomic DNA
1335         (ix) FEATURE:
1336             (A) NAME/KEY: smage-I
1337         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
1338
1339
1340
1341 TCTGTCTGCA TATGCCTCCA CTTGTGTGTA GCAGTCTCAA ATGGATCTCT      50
1342 CTCTACAGAC CTCTGTCTGT GTCTGGCACC CTAAGTGGCT TTGCATGGGC      100
1343 ACAGGTTTCT GCCCCTGCAT GGAGCTTAAA TAGATCTTTC TCCACAGGCC      150
1344 TATACCCCTG CATTGTAAGT TTAAGTGGCT TTATGTGGAT ACAGGTCTCT      200
1345 GCCCTTGTAT GCAGGCCTAA GTTTTCTGT CTGCTTAACC CCTCCAAGTG      250
1346 AAGCTAGTGA AAGATCTAAC CCACCTTTTG AAGTCTGAAA CTAGACTTTT      300
1347 ATGCAGTGGC CTAACAAGTT TTAATTTCTT CCACAGGGTT TGCAGAAAAG      350
1348 AGCTTGATCC ACGAGTTCAG AAGTCCTGGT ATGTTCTTAG AAAG          394
1349 ATG TTC TCC TGG AAA GCT TCA AAA GCC AGG TCT CCA TTA AGT      436
1350 CCA AGG TAT TCT CTA CCT GGT AGT ACA GAG GTA CTT ACA GGT      478
1351 TGT CAT TCT TAT CCT TCC AGA TTC CTG TCT GCC AGC TCT TTT      520
1352 ACT TCA GCC CTG AGC ACA GTC AAC ATG CCT AGG GGT CAA AAG      562
1353 AGT AAG ACC CGC TCC CGT GCA AAA CGA CAG CAG TCA CGC AGG      604
1354 GAG GTT CCA GTA GTT CAG CCC ACT GCA GAG GAA GCA GGG TCT      646
1355 TCT CCT GTT GAC CAG AGT GCT GGG TCC AGC TTC CCT GGT GGT      688
1356 TCT GCT CCT CAG GGT GTG AAA ACC CCT GGA TCT TTT GGT GCA      730
1357 GGT GTA TCC TGC ACA GGC TCT GGT ATA GGT GGT AGA AAT GCT      772
1358 GCT GTC CTG CCT GAT ACA AAA AGT TCA GAT GGC ACC CAG GCA      814
1359 GGG ACT TCC ATT CAG CAC ACA CTG AAA GAT CCT ATC ATG AGG      856
1360 AAG GCT AGT GTG CTG ATA GAA TTC CTG CTA GAT AAA TTT AAG      898
1361 ATG AAA GAA GCA GTT ACA AGG AGT GAA ATG CTG GCA GTA GTT      940
1362 AAC AAG AAG TAT AAG GAG CAA TTC CCT GAG ATC CTC AGG AGA      982
1363 ACT TCT GCA CGC CTA GAA TTA GTC TTT GGT CTT GAG TTG AAG      1024
1364 GAA ATT GAT CCC AGC ACT CAT TCC TAT TTG CTG GTA GGC AAA      1066
1365 CTG GGT CTT TCC ACT GAG GGA AGT TTG AGT AGT AAC TGG GGG      1108
1366 TTG CCT AGG ACA GGT CTC CTA ATG TCT GTC CTA GGT GTG ATC      1150
1367 TTC ATG AAG GGT AAC CGT GCC ACT GAG CAA GAG GTC TGG CAA      1192
1368 TTT CTG CAT GGA GTG GGG GTA TAT GCT GGG AAG AAG CAC TTG      1234
1369 ATC TTT GGC GAG CCT GAG GAG TTT ATA AGA GAT GTA GTG CGG      1276
1370 GAA AAT TAC CTG GAG TAC CGC CAG GTA CCT GGC AGT GAT CCC      1318
1371 CCA AGC TAT GAG TTC CTG TGG GGA CCC AGA GCC CAT GCT GAA      1360
1372 ACA ACC AAG ATG AAA GTC CTG GAA GTT TTA GCT AAA GTC AAT      1402
1373 GGC ACA GTC CCT AGT GCC TTC CCT AAT CTC TAC CAG TTG GCT      1444
1374 CTT AGA GAT CAG GCA GGA GGG GTG CCA AGA AGG AGA GTT CAA      1486
1375 GGC AAG GGT GTT CAT TCC AAG GCC CCA TCC CAA AAG TCC TCT      1528
1376 AAC ATG TAG          1537
1377 TTGAGTCTGT TCTGTTGTGT TTGAAAAACA GTCAGGCTCC TAATCAGTAG      1587
1378 AGAGTTCATA GCCTACCAGA ACCAACATGC ATCCATTCTT GGCCGTGTTAT      1637
1379 ACATTAGTAG AATGGAGGCT ATTTTGTGTA CTTTTCAAAT GTTTGTTTAA      1687
1380 CTAAACAGTG CTTTTTGCCA TGCTTCTTGT TAACTGCATA AAGAGGTAAC      1737
1381 TGTCACCTGT CAGATTAGGA CTTGTTTTGT TATTTGCAAC AAAGTGAAGT      1787
1382 ACATTATTTT GTTTTTACTA AAACATTGTG TAACATTGCA TTGGAGAAGG      1837
1383 GATTGTCATG GCAATGTGAT ATCATACAGT GGTGAAACAA CAGTGAAGTG      1887
1384 GGAAAGTTTA TATTGTAAAT TTTGAAAATT TTATGAGTGT GATTGCTGTA      1937
1385 TACTTTTTTC TTTTTTGTAT AATGCTAAGT GAAATAAAGT TGGATTTGAT      1987

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RAW SEQUENCE LISTING
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1386	GACTTTACTC	AAATTCATTA	GAAAGTAAAT	CGTAAAACTC	TATTACTTTA	2037
1387	TTATTTTCTT	CAATTATGAA	TTAAGCATTG	GTTATCTGGA	AGTTTCTCCA	2087
1388	GTAGCACAGG	ATCTAGTATG	AAATGTATCT	AGTATAGGCA	CTGACAGTGA	2137
1389	GTTATCAGAG	TCT				2150
1390						
1391						
1392						

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SEQUENCE VERIFICATION REPORT
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Line	Error	Original Text
31	Wrong Classification	(C) CLASSIFICATION: 435